



Transcriptome and Metabolome Analysis to Characterize Cold Stress in walnuts (*Juglans regia* L.)

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Summary: We studied the microstructure changes, electrical conductivity, antioxidant enzyme activity, transcriptome and metabolome with 'Qingxiang' and 'Liao No.8' leaves samples grafted on the same rootstock under cold stress. The transcriptome data showed that a total of 6458 differentially expressed genes (DEG) were identified in 'Qingxiang', and 3635 DEGs were identified in 'Liao No.8' were identified, and pathway enrichments were analyzed; base on metabolome 83 differentially expressed metabolites in 'Qingxiang' and 216 differentially expressed metabolites in 'Liao No.8', with analyzed its metabolic enrichment pathway. Importantly, the degree of metabolite expression changes in 'Liao No.8' was usually much more pronounced than in 'Qingxiang', which may help explain the excellent cold tolerance of 'Liao No.8'. Significantly related genes and metabolites were found in the results of the conjoint analysis of the transcriptome and metabolome, which will help us to discover the key genes and metabolites in response to cold stress, but the specific mechanism of action needs to be further studied.

